

SEQUENCE LISTING



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KELLY, SUSAN J.

<120> URATE OXIDASE

<130> 1579-379

<140> PCT/US99/17678

<141> 1999-08-05

<160>13

<170> PatentIn Ver. 2.0

<210> 1

<211> 915

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(915)

<220>

<223> Description of Artificial Sequence:PBC CHIMERA

<400> 1

atg gct cat tac cgt aat gac tac aaa aag aat gat gag gta gag ttt	48
Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe	
1 5 10 15	
gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag	96
Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln	
20 25 30	
cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa	144
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	
35 40 45	
ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat	192
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	
50 55 60	
gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag	240
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	
65 70 75 80	
ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag	288
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu	
85 90 95	
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg	336
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val	
100 105 110	
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc	384
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val	
115 120 125	
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa	432
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu	
130 135 140	
cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta	480

Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu	
145					150					155					160	
aaa	gtc	ttg	aaa	aca	acc	cag	tct	ggc	ttt	gaa	gga	ttc	atc	aag	gac	528
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp	
				165				170						175		
cag	ttc	acc	acc	ctc	cct	gag	gtg	aag	gac	cgg	tgc	ttt	gcc	acc	caa	576
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln	
				180				185					190			
gtg	tac	tgc	aaa	tgg	cgc	tac	cac	cag	ggc	aga	gat	gtg	gac	ttt	gag	624
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu	
		195					200					205				
gcc	acc	tgg	gac	act	gtt	agg	agc	att	gtc	ctg	cag	aaa	ttt	gct	ggg	672
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly	
		210				215					220					
ccc	tat	gac	aaa	ggc	gag	tac	tca	ccc	tct	gtg	cag	aag	acc	ctc	tat	720
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr	
225				230						235					240	
gat	atc	cag	gtg	ctc	tcc	ctg	agc	cga	gtt	cct	gag	ata	gaa	gat	atg	768
Asp	Ile	Gln	Val	Leu	Ser	Leu	Ser	Arg	Val	Pro	Glu	Ile	Glu	Asp	Met	
				245					250					255		
gaa	atc	agc	ctg	cca	aac	att	cac	tac	ttc	aat	ata	gac	atg	tcc	aaa	816
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys	
			260					265					270			
atg	ggc	ctg	atc	aac	aag	gaa	gag	gtc	ttg	ctg	cca	tta	gac	aat	cca	864
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro	
		275					280					285				
tat	gga	aaa	att	act	ggc	aca	gtc	aag	agg	aag	ttg	tct	tca	aga	ctg	912
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu	
		290				295					300					
tga																915

<210> 2

<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PBC CHIMERA

<400> 2

Met	Ala	His	Tyr	Arg	Asn	Asp	Tyr	Lys	Lys	Asn	Asp	Glu	Val	Glu	Phe
1				5					10					15	

Val	Arg	Thr	Gly	Tyr	Gly	Lys	Asp	Met	Ile	Lys	Val	Leu	His	Ile	Gln
			20					25					30		

Arg	Asp	Gly	Lys	Tyr	His	Ser	Ile	Lys	Glu	Val	Ala	Thr	Ser	Val	Gln
		35					40					45			

Leu	Thr	Leu	Ser	Ser	Lys	Lys	Asp	Tyr	Leu	His	Gly	Asp	Asn	Ser	Asp
	50					55					60				

Val	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	Asn	Val	Leu	Ala	Lys
65					70					75					80

Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu	
				85					90					95		
His	Phe	Leu	Ser	Ser	Phe	Lys	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val	
			100					105					110			
Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val	
		115					120					125				
His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu	
	130					135					140					
Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu	
145					150					155					160	
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp	
			165						170					175		
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln	
			180					185					190			
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu	
		195					200					205				
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly	
	210					215					220					
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr	
225					230					235					240	
Asp	Ile	Gln	Val	Leu	Ser	Leu	Ser	Arg	Val	Pro	Glu	Ile	Glu	Asp	Met	
			245						250					255		
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys	
			260					265					270			
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro	
	275						280					285				
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu	
	290					295					300					

<210> 3

<211> 915

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(915)

<220>

<223> Description of Artificial Sequence:pks chimera

<400> 3

atg	gct	cat	tac	cgt	aat	gac	tac	aaa	aag	aat	gat	gag	gta	gag	ttt	48
Met	Ala	His	Tyr	Arg	Asn	Asp	Tyr	Lys	Lys	Asn	Asp	Glu	Val	Glu	Phe	
1				5					10					15		

gtc	cga	act	ggc	tat	ggg	aag	gat	atg	ata	aaa	gtt	ctc	cat	att	cag	96
Val	Arg	Thr	Gly	Tyr	Gly	Lys	Asp	Met	Ile	Lys	Val	Leu	His	Ile	Gln	
			20					25					30			

cga	gat	gga	aaa	tat	cac	agc	att	aaa	gag	gtg	gca	act	tca	gtg	caa	144
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Arg	Asp	Gly	Lys	Tyr	His	Ser	Ile	Lys	Glu	Val	Ala	Thr	Ser	Val	Gln	
		35					40					45				
ctg	act	ttg	agc	tcc	aaa	aaa	gat	tac	ctg	cat	gga	gac	aat	tca	gat	192
Leu	Thr	Leu	Ser	Ser	Lys	Lys	Asp	Tyr	Leu	His	Gly	Asp	Asn	Ser	Asp	
	50					55					60					
gtc	atc	cct	aca	gac	acc	atc	aag	aac	aca	gtt	aat	gtc	ctg	gcg	aag	240
Val	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	Asn	Val	Leu	Ala	Lys	
	65				70					75					80	
ttc	aaa	ggc	atc	aaa	agc	ata	gaa	act	ttt	gct	gtg	act	atc	tgt	gag	288
Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu	
				85					90					95		
cat	ttc	ctt	tct	tcc	ttc	aag	cat	gtc	atc	aga	gct	caa	gtc	tat	gtg	336
His	Phe	Leu	Ser	Ser	Phe	Lys	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val	
			100					105					110			
gaa	gaa	gtt	cct	tgg	aag	cgt	ttt	gaa	aag	aat	gga	gtt	aag	cat	gtc	384
Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val	
		115					120					125				
cat	gca	ttt	att	tat	act	cct	act	gga	acg	cac	ttc	tgt	gag	gtt	gaa	432
His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu	
	130					135					140					
cag	ata	agg	aat	gga	cct	cca	gtc	att	cat	tct	gga	atc	aaa	gac	cta	480
Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu	
	145				150					155					160	
aaa	gtc	ttg	aaa	aca	acc	cag	tct	ggc	ttt	gaa	gga	ttc	atc	aag	gac	528
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp	
				165				170						175		
cag	ttc	acc	acc	ctc	cct	gag	gtg	aag	gac	cgg	tgc	ttt	gcc	acc	caa	576
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln	
			180					185					190			
gtg	tac	tgc	aaa	tgg	cgc	tac	cac	cag	ggc	aga	gat	gtg	gac	ttt	gag	624
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu	
		195					200					205				
gcc	acc	tgg	gac	act	gtt	agg	agc	att	gtc	ctg	cag	aaa	ttt	gct	ggg	672
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly	
	210					215					220					
ccc	tat	gac	aaa	ggc	gag	tac	tcg	ccc	tct	gtc	cag	aag	aca	ctc	tat	720
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr	
	225				230					235					240	
gac	atc	cag	gtg	ctc	acc	ctg	ggc	cag	gtt	cct	gag	ata	gaa	gat	atg	768
Asp	Ile	Gln	Val	Leu	Thr	Leu	Gly	Gln	Val	Pro	Glu	Ile	Glu	Asp	Met	
				245				250						255		
gaa	atc	agc	ctg	cca	aat	att	cac	tac	tta	aac	ata	gac	atg	tcc	aaa	816
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Leu	Asn	Ile	Asp	Met	Ser	Lys	
			260					265					270			
atg	gga	ctg	atc	aac	aag	gaa	gag	gtc	ttg	cta	cct	tta	gac	aat	cca	864
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro	
		275					280					285				
tat	gga	aaa	att	act	ggc	aca	gtc	aag	agg	aag	ttg	tct	tca	aga	ctg	912
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu	
	290					295					300					

<210> 4  
 <211> 304  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:pks chimera

<400> 4  
 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe  
   1                  5                  10                  15  
 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln  
                   20                  25                  30  
 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
                   35                  40                  45  
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
   50                  55                  60  
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
   65                  70                  75                  80  
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu  
                   85                  90                  95  
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val  
                   100                  105                  110  
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val  
                   115                  120                  125  
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
   130                  135                  140  
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
   145                  150                  155                  160  
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
                   165                  170                  175  
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
                   180                  185                  190  
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
                   195                  200                  205  
 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly  
   210                  215                  220  
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
   225                  230                  235                  240  
 Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met  
                   245                  250                  255  
 Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys  
                   260                  265                  270  
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro

275	280	285
Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu		
290	295	300

<210> 5  
 <211> 304  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: baboon D3H

<400> 5  
 Met Ala His Tyr His Asn Asn Tyr Lys Lys Asn Asp Glu Leu Glu Phe  
 1 5 10 15  
 Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln  
 20 25 30  
 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
 35 40 45  
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
 50 55 60  
 Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys  
 65 70 75 80  
 Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu  
 85 90 95  
 Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val  
 100 105 110  
 Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val  
 115 120 125  
 His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
 130 135 140  
 Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
 145 150 155 160  
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
 165 170 175  
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
 180 185 190  
 Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu  
 195 200 205  
 Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly  
 210 215 220  
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
 225 230 235 240  
 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met  
 245 250 255  
 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys  
 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu  
290 295 300

<210> 6  
<211> 304  
<212> PRT  
<213> baboon

<400> 6  
Met Ala Asp Tyr His Asn Asn Tyr Lys Lys Asn Asp Glu Leu Glu Phe  
1 5 10 15  
Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln  
20 25 30  
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
35 40 45  
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
50 55 60  
Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys  
65 70 75 80  
Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu  
85 90 95  
Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val  
100 105 110  
Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val  
115 120 125  
His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
130 135 140  
Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
145 150 155 160  
Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
165 170 175  
Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
180 185 190  
Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu  
195 200 205  
Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly  
210 215 220  
Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
225 230 235 240  
Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met  
245 250 255  
Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys  
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu  
290 295 300

<210> 7  
<211> 304  
<212> PRT  
<213> pig

<400> 7  
Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe  
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln  
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu  
85 90 95

His Phe Leu Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val  
100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val  
115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly  
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met  
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys



260	265	270
Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro		
275	280	285
Tyr Gly Arg Ile Thr Gly Thr Val Lys Arg Lys Leu Thr Ser Arg Leu		
290	295	300

<210> 8  
 <211> 298  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PBC amino truncated

<400> 8  
 Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly  
 1 5 10 15  
 Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His  
 20 25 30  
 Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys  
 35 40 45  
 Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr  
 50 55 60  
 Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser  
 65 70 75 80  
 Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe  
 85 90 95  
 Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys  
 100 105 110  
 Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr  
 115 120 125  
 Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro  
 130 135 140  
 Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr  
 145 150 155 160  
 Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro  
 165 170 175  
 Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg  
 180 185 190  
 Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val  
 195 200 205  
 Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu  
 210 215 220  
 Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Ser  
 225 230 235 240

Leu Ser Arg Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn  
 245 250 255  
 Ile His Tyr Phe Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys  
 260 265 270  
 Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly  
 275 280 285  
 Thr Val Lys Arg Lys Leu Ser Ser Arg Leu  
 290 295

<210> 9  
 <211> 301  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PBC carboxy truncated

<400> 9  
 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe  
 1 5 10 15  
 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln  
 20 25 30  
 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
 35 40 45  
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
 50 55 60  
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
 65 70 75 80  
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu  
 85 90 95  
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val  
 100 105 110  
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val  
 115 120 125  
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
 130 135 140  
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
 145 150 155 160  
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
 165 170 175  
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
 180 185 190  
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
 195 200 205  
 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly  
 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
 225 230 235 240  
 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met  
 245 250 255  
 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys  
 260 265 270  
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
 275 280 285  
 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser  
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<210> 10

<211> 298

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PKS amino truncated

<400> 10

Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly  
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 Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His  
 20 25 30  
 Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys  
 35 40 45  
 Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr  
 50 55 60  
 Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser  
 65 70 75 80  
 Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe  
 85 90 95  
 Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys  
 100 105 110  
 Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr  
 115 120 125  
 Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro  
 130 135 140  
 Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr  
 145 150 155 160  
 Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro  
 165 170 175  
 Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg  
 180 185 190  
 Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val  
 195 200 205

Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu  
 210 215 220  
 Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Thr  
 225 230 235 240  
 Leu Gly Gln Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn  
 245 250 255  
 Ile His Tyr Leu Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys  
 260 265 270  
 Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly  
 275 280 285  
 Thr Val Lys Arg Lys Leu Ser Ser Arg Leu  
 290 295

<210> 11  
 <211> 301  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PKS carboxy truncated

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 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe  
 1 5 10 15  
 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln  
 20 25 30  
 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
 35 40 45  
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
 50 55 60  
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
 65 70 75 80  
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu  
 85 90 95  
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val  
 100 105 110  
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val  
 115 120 125  
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
 130 135 140  
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
 145 150 155 160  
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
 165 170 175  
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly  
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met  
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys  
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser  
290 295 300

<210> 12  
<211> 915  
<212> DNA  
<213> PIG

<400> 12  
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tatgggaagg atatgataaa agttctccat attcagcgag atggaaaata tcacagcatt 120  
aaagagggtgg caacttcagt gcaactgact ttgagctcca aaaaagatta cctgcatgga 180  
gacaattcag atgtcatccc tacagacacc atcaagaaca cagttaatgt cctggcgaag 240  
ttcaaaggca tcaaaagcat agaaactttt gctgtgacta tctgtgagca tttcctttct 300  
tccttcaagc atgtcatcag agctcaagtc tatgtggaag aagttccttg gaagcgtttt 360  
gaaaagaatg gagttaagca tgtccatgca tttatttata ctccacttg aacgcacttc 420  
tgtgaggttg aacagataag gaatggacct ccagtcattc attctggaat caaagaccta 480  
aaagtcttga aaacaaccca gtctggcttt gaaggattca tcaaggacca gttcaccacc 540  
ctccctgagg tgaaggaccg gtgctttgcc acccaagtgt actgcaaag ggcgtaccac 600  
cagggcagag atgtggactt tgaggccacc tgggacactg ttaggagcat tgtcctgcag 660  
aaatttgctg ggccctatga caaaggcgag tactcgccct ctgtccagaa gacactctat 720  
gacatccagg tgctcaccct gggccagggt cctgagatag aagatatgga aatcagcctg 780  
ccaaatattc actacttaaa catagacatg tccaaaatgg gactgatcaa caaggaagag 840  
gtcttgctac ctttagacaa tccatatggc aggattactg gtacagtcaa gaggaagctg 900  
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<210> 13  
<211> 915  
<212> DNA  
<213> BABOON

<400> 13  
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tatgggaagg atatggtaaa agttctccat attcagcgag atggaaaata tcacagcatt 120  
aaagagggtgg caacttcagt gcaacttact ctgagttcca aaaaagatta cctgcatgga 180  
gataattcag atatcatccc tacagacacc atcaagaaca cagttcatgt cttggcaaaag 240  
tttaaggga tcaaaagcat agaagccttt ggtgtgaata tttgtgagta ttttctttct 300  
tcttttaacc atgtaatccg agctcaagtc tacgtggaag aaatcccttg gaagcgctct 360  
gaaaagaatg gagttaagca tgtccatgca tttattcaca ctcccacttg aacacacttc 420  
tgtgaagttg aacaactgag aagtggaccc cccgtcattc attctggaat caaagacctc 480  
aaggtcttga aaacaacaca gtctggattt gaaggtttca tcaaggacca gttcaccacc 540  
ctccctgagg tgaaggaccg atgctttgcc acccaagtgt actgcaagtg gcgctaccac 600  
cagtgcaggg atgtggactt cgaggctacc tggggcacca ttcgggacct tgtcctggag 660  
aaatttgctg ggccctatga caaaggcgag tactcaccct ctgtgcagaa gaccctctat 720  
gatatccagg tgctctccct gagccgagtt cctgagatag aagatatgga aatcagcctg 780

ccaaacattc actacttcaa tatagacatg tccaaaatgg gtctgatcaa caaggaagag 840  
gtcttgctgc cattagacaa tccatatgga aaaattactg gtacagtcaa gaggaagttg 900  
tcttcaagac tgtga 915